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1653

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/827,110A

DATE: 02/11/2002
TIME: 13:36:25

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Output Set: N:\CRF3\02112002\I827110A.raw

ENTERED

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   3  <110> APPLICANT: Wang, Elizabeth
   5  <120> TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
   6        POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
   8  <130> FILE REFERENCE: CIBT-P03-031
C--> 10  <140> CURRENT APPLICATION NUMBER: US/09/827,110A
C--> 11  <141> CURRENT FILING DATE: 2001-04-05
  13  <150> PRIOR APPLICATION NUMBER: 08/955,552
  14  <151> PRIOR FILING DATE: 1997-10-20
  16  <160> NUMBER OF SEQ ID NOS: 28
  18  <170> SOFTWARE: PatentIn Ver. 2.0
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  21  <211> LENGTH: 1277
  22  <212> TYPE: DNA
  23  <213> ORGANISM: chicken Shh
  25  <220> FEATURE:
  26  <221> NAME/KEY: CDS
  27  <222> LOCATION: (1)..(1275)
  29  <400> SEQUENCE: 1
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  31  Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile
  32  1               5                  10                  15
  34  tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc   96
  35  Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly
  36                 20                  25                  30
  38  att gga aaa agg agg cac ccc aaa aag ctg acc ccg tta gcc tat aag  144
  39  Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
  40             35                  40                  45
  42  cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga  192
  43  Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg
  44         50                  55                  60
  46  tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc  240
  47  Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr
  48  65                  70                  75                  80
  50  cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga  288
  51  Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly
  52                 85                  90                  95
  54  gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg  336
  55  Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu
  56             100                 105                 110
  58  gcg atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc  384
  59  Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr
  60             115                 120                 125
  62  gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac  432
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63  Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr
64      130             135             140
66  gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag    480
67  Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
68  145             150             155             160
70  tac gga atg ctg gcc cgc ctc gcc gtc gag gcc ggc ttc gac tgg gtc    528
71  Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
72              165             170             175
74  tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac    576
75  Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
76              180             185             190
78  tca gtg gca gcg aaa tca gga ggc tgc ttc cct ggc tca gcc aca gtg    624
79  Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
80              195             200             205
82  cac ctg gag cat gga ggc acc aag ctg gtg aag gac ctg agc cct ggg    672
83  His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
84      210             215             220
86  gac cgc gtg ctg gct gct gac gcg gac ggc cgg ctg ctc tac agt gac    720
87  Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
88  225             230             235             240
90  ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac    768
91  Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
92              245             250             255
94  gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc    816
95  Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
96              260             265             270
98  cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcg gag gcc aca ggg    864
99  His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
100         275             280             285
102 tcc acc agt ggc cag gcg ctc ttc gcc agc aac gtg aag cct ggc caa    912
103 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
104     290             295             300
106 cgt gtc tat gtg ctg ggc gag ggc ggg cag cag ctg ctg ccg gcg tct    960
107 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
108 305             310             315             320
110 gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca   1008
111 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
112             325             330             335
114 ctc acc gcc cag ggc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc   1056
115 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
116             340             345             350
118 tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca   1104
119 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
120     355             360             365
122 ttc cgc ttg gct cag ggg ctg ctg gcc gcc ctc tgc cca gat ggg gcc   1152
123 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
124     370             375             380
126 atc cct act gcc gcc acc acc acc act ggc atc cat tgg tac tca cgg   1200
127 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
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128 385                  390                  395                  400
130 ctc ctc tac cgc atc ggc agc tgg gtg ctg gat ggt gac gcg ctg cat   1248
131 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
132                  405                  410                  415
134 ccg ctg ggc atg gtg gca ccg gcc agc tg                            1277
135 Pro Leu Gly Met Val Ala Pro Ala Ser
136                  420                  425
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 1190
140 <212> TYPE: DNA
141 <213> ORGANISM: murine Dhh
143 <220> FEATURE:
144 <221> NAME/KEY: CDS
145 <222> LOCATION: (1)..(1188)
147 <400> SEQUENCE: 2
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150 1                  5                  10                  15
152 gca cta tct gcc cag agc tgc ggg ccg ggc cga gga ccg gtt ggc cgg   96
153 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
154                  20                  25                  30
156 cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt   144
157 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
158            35                  40                  45
160 gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag   192
161 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
162       50                  55                  60
164 ggg agg gta aca agg ggg tcg gag cgc ttc cgg gac ctc gta ccc aac   240
165 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
166 65                  70                  75                  80
168 tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac   288
169 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
170                  85                  90                  95
172 cgc ctg atg aca gag cgt tgc aaa gag cgg gtg aac gct cta gcc atc   336
173 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
174            100                 105                 110
176 gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc   384
177 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
178            115                 120                 125
180 tgg gac gag gac ggc cac cac gca cag gat tca ctc cac tac gaa ggc   432
181 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
182       130                 135                 140
184 cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt   480
185 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
186 145                 150                 155                 160
188 ttg ttg gcg cgc cta gct gtg gaa gcc gga ttc gac tgg gtc tac tac   528
189 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
190                 165                 170                 175
192 gag tcc cgc aac cac atc cac gta tcg gtc aaa gct gat aac tca ctg   576
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193 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
194             180             185             190
196 gcg gtc cga gcc gga ggc tgc ttt ccg gga aat gcc acg gtg cgc ttg    624
197 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
198         195             200             205
200 cgg agc ggc gaa cgg aag ggg ctg agg gaa cta cat cgt ggt gac tgg    672
201 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
202     210             215             220
204 gta ctg gcc gct gat gca gcg ggc cga gtg gta ccc acg cca gtg ctg    720
205 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
206 225             230             235             240
208 ctc ttc ctg gac cgg gat ctg cag cgc cgc gcc tcg ttc gtg gct gtg    768
209 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
210             245             250             255
212 gag acc gag cgg cct ccg cgc aaa ctg ttg ctc aca ccc tgg cat ctg    816
213 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
214             260             265             270
216 gtg ttc gct gct cgc ggg cca gcg cct gct cca ggt gac ttt gca ccg    864
217 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
218         275             280             285
220 gtg ttc gcg cgc cgc tta cgt gct ggc gac tcg gtg ctg gct ccc ggc    912
221 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
222     290             295             300
224 ggg gac gcg ctc cag ccg gcg cgc gta gcc cgc gtg gcg cgc gag gaa    960
225 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
226 305             310             315             320
228 gcc gtg ggc gtg ttc gca ccg ctc act gcg cac ggg acg ctg ctg gtc   1008
229 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
230             325             330             335
232 aac gac gtc ctc gcc tcc tgc tac gcg gtt cta gag agt cac cag tgg   1056
233 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
234             340             345             350
236 gcc cac cgc gcc ttc gcc cct ttg cgg ctg ctg cac gcg ctc ggg gct   1104
237 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
238             355             360             365
240 ctg ctc cct ggg ggt gca gtc cag ccg act ggc atg cat tgg tac tct   1152
241 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
242     370             375             380
244 cgc ctc ctt tac cgc ttg gcc gag gag tta atg ggc tg                1190
245 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
246 385             390             395
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249 <211> LENGTH: 1281
250 <212> TYPE: DNA
251 <213> ORGANISM: murine Ihh
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254 <221> NAME/KEY: CDS
255 <222> LOCATION: (1)..(1233)
257 <400> SEQUENCE: 3
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260   1               5                  10             15
262 ctg ctg ctg ctt ctg gtg ccg gcg gcg cgg ggc tgc ggg ccg ggc cgg    96
263 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
264             20                  25                  30
266 gtg gtg ggc agc cgc cgg agg ccg cct cgc aag ctc gtg cct ctt gcc   144
267 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
268             35                  40                  45
270 tac aag cag ttc agc ccc aac gtg ccg gag aag acc ctg ggc gcc agc   192
271 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
272     50                  55                  60
274 ggg cgc tac gaa ggc aag atc gcg cgc agc tct gag cgc ttc aaa gag   240
275 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
276   65                  70                  75                  80
278 ctc acc ccc aac tac aat ccc gac atc atc ttc aag gac gag gag aac   288
279 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
280                     85                  90                  95
282 acg ggt gcc gac cgc ctc atg acc cag cgc tgc aag gac cgt ctg aac   336
283 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
284             100                 105                 110
286 tca ctg gcc atc tct gtc atg aac cag tgg cct ggt gtg aaa ctg cgg   384
287 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
288             115                 120                 125
290 gtg acc gaa ggc cgg gat gaa gat ggc cat cac tca gag gag tct tta   432
291 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
292     130                 135                 140
294 cac tat gag ggc cgc gcg gtg gat atc acc acc tca gac cgt gac cga   480
295 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
296 145                 150                 155                 160
298 aat aag tat gga ctg ctg gcg cgc tta gca gtg gag gcc ggc ttc gac   528
299 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
300                 165                 170                 175
302 tgg gtg tat tac gag tcc aag gcc cac gtg cat tgc tct gtc aag tct   576
303 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
304             180                 185                 190
306 gag cat tcg gcc gct gcc aag aca ggt ggc tgc ttt cct gcc gga gcc   624
307 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
308             195                 200                 205
310 cag gtg cgc cta gag aac ggg gag cgt gtg gcc ctg tca gct gta aag   672
311 Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
312     210                 215                 220
314 cca gga gac cgg gtg ctg gcc atg ggg gag gat ggg acc ccc acc ttc   720
315 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
316 225                 230                 235                 240
318 agt gat gtg ctt att ttc ctg gac cgc gag cca aac cgg ctg aga gct   768
319 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
320                 245                 250                 255
322 ttc cag gtc atc gag act cag gat cct ccg cgt cgg ctg gcg ctc acg   816
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

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                       VERIFICATION SUMMARY            DATE: 02/11/2002
                       PATENT APPLICATION:  US/09/827,110A    TIME: 13:36:26

                       Input Set : A:\8575959.txt
                       Output Set: N:\CRF3\02112002\I827110A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1615 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:1615 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:1615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2216 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:2216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2222 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:2222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2231 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:2231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:2234 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
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